

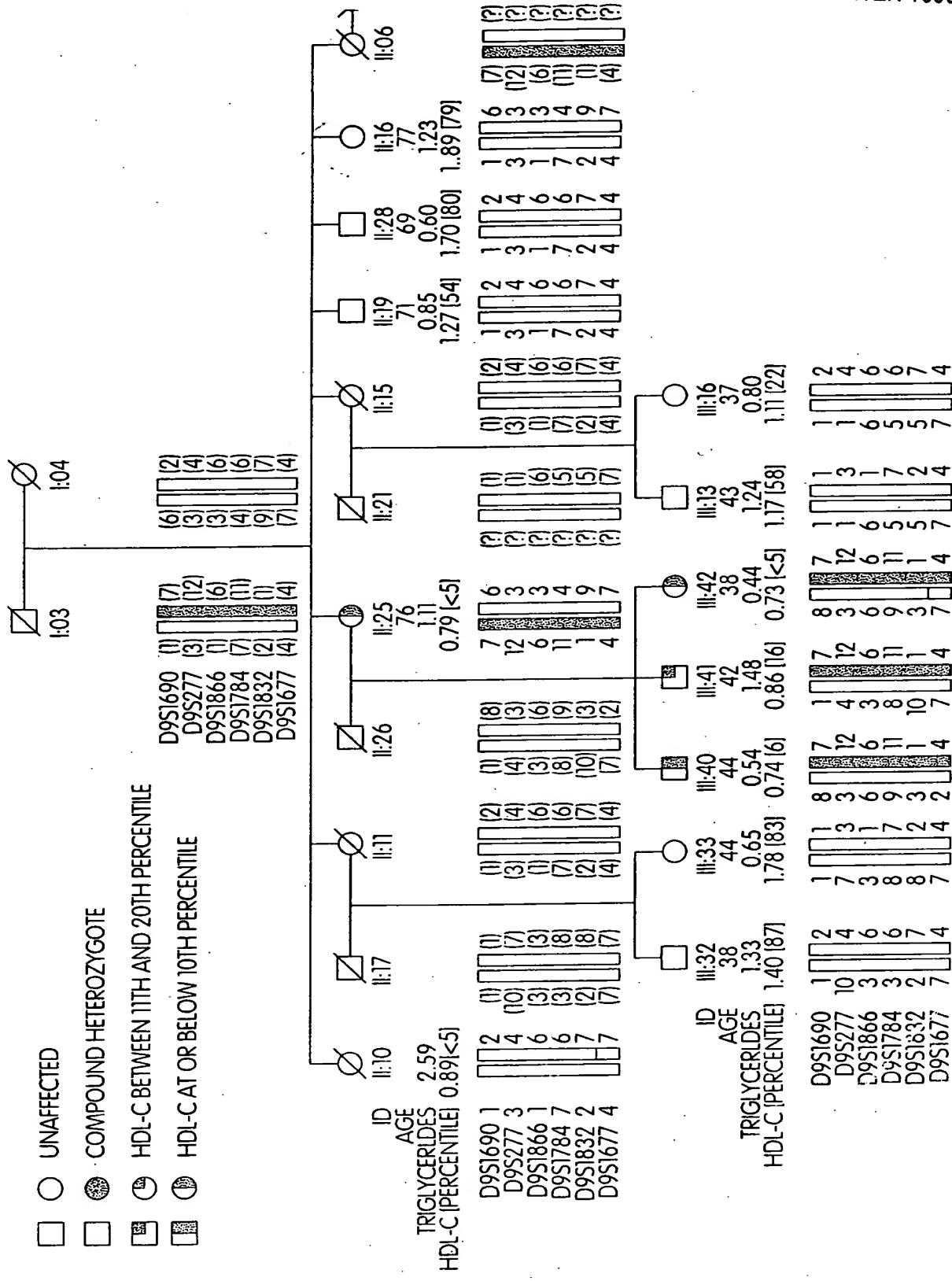


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**Figure 1A**

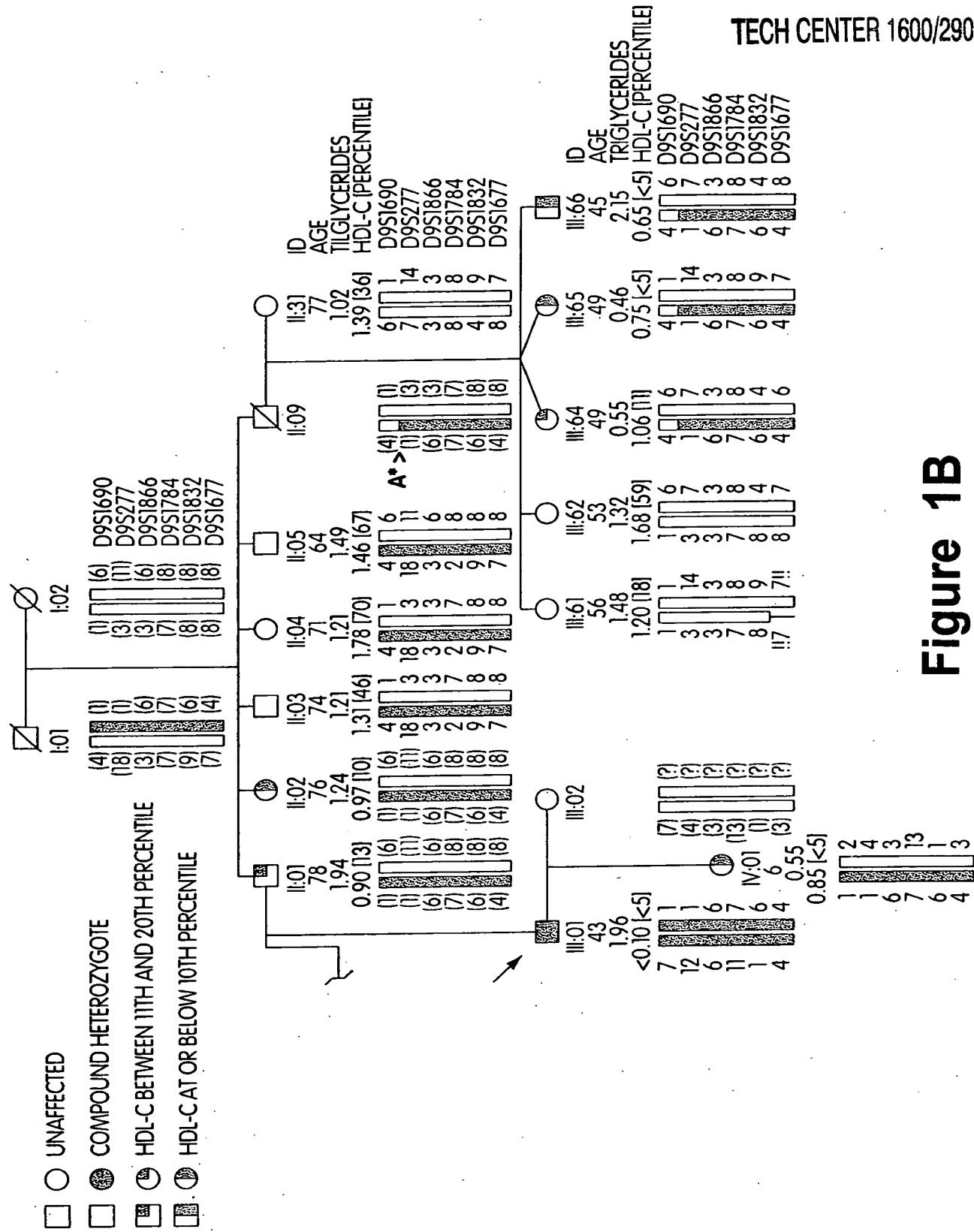


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**Figure 1B**



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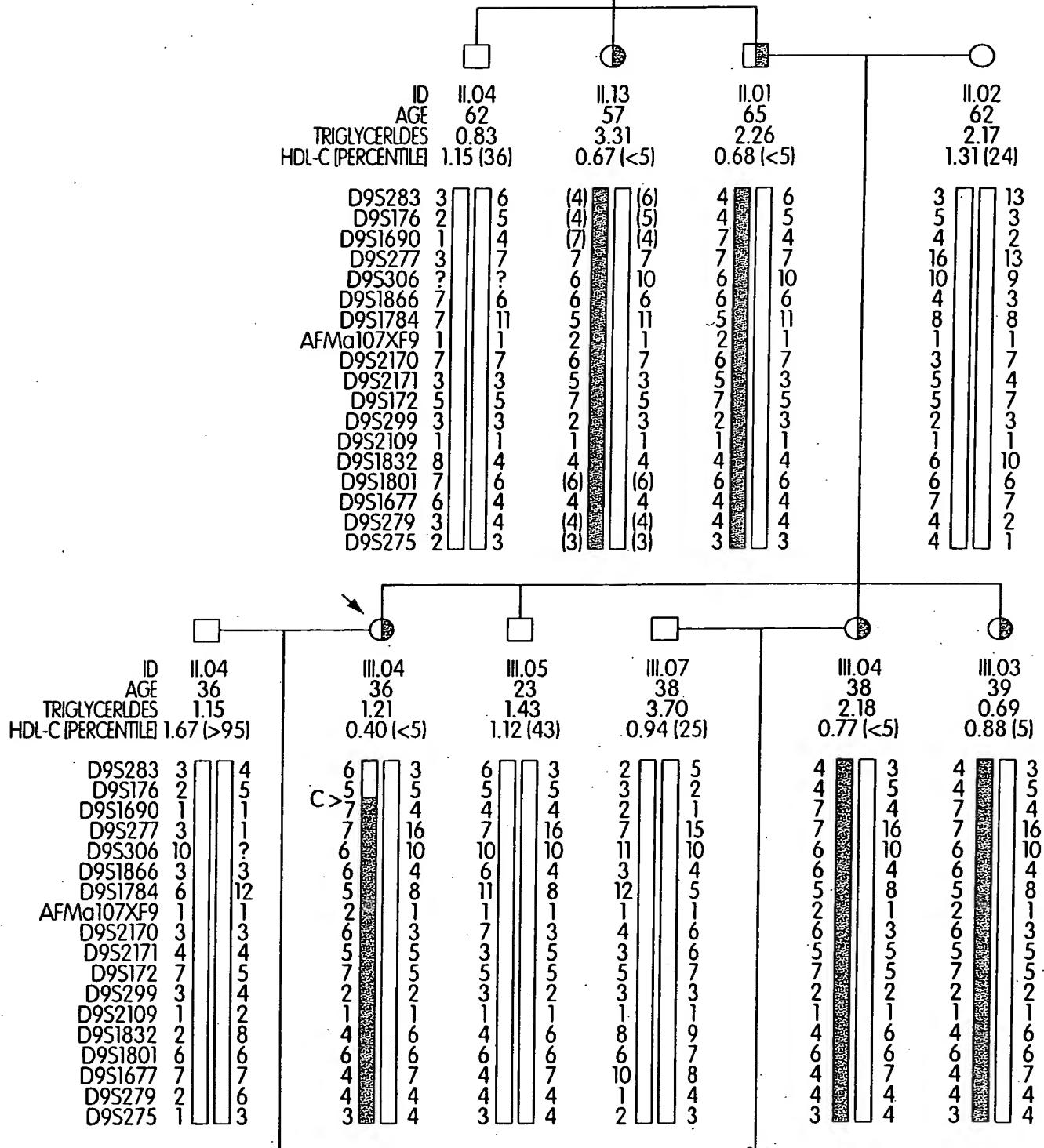


Figure 2A - (1)



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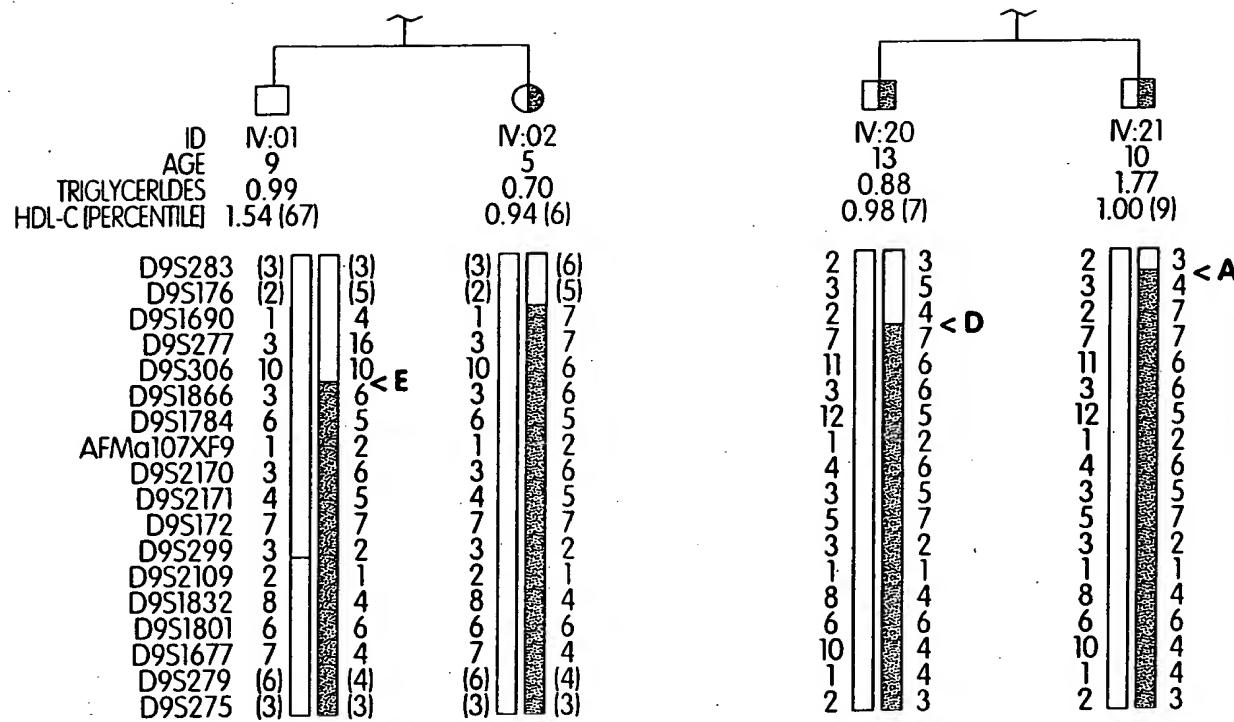
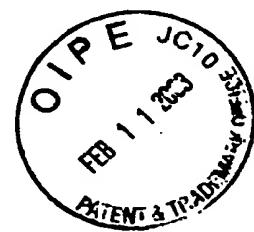


Figure 2A – (2)



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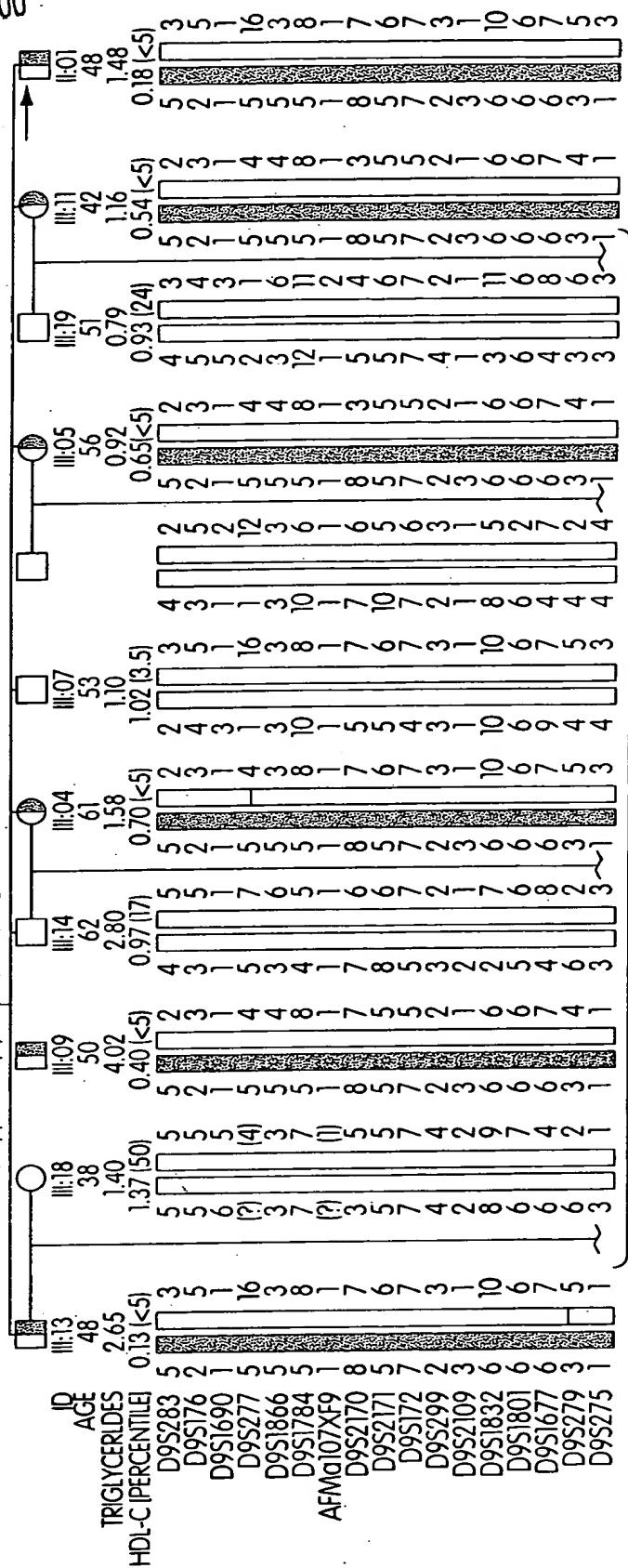
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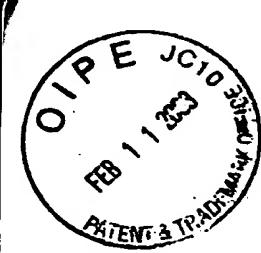
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Figure 2B - (1)





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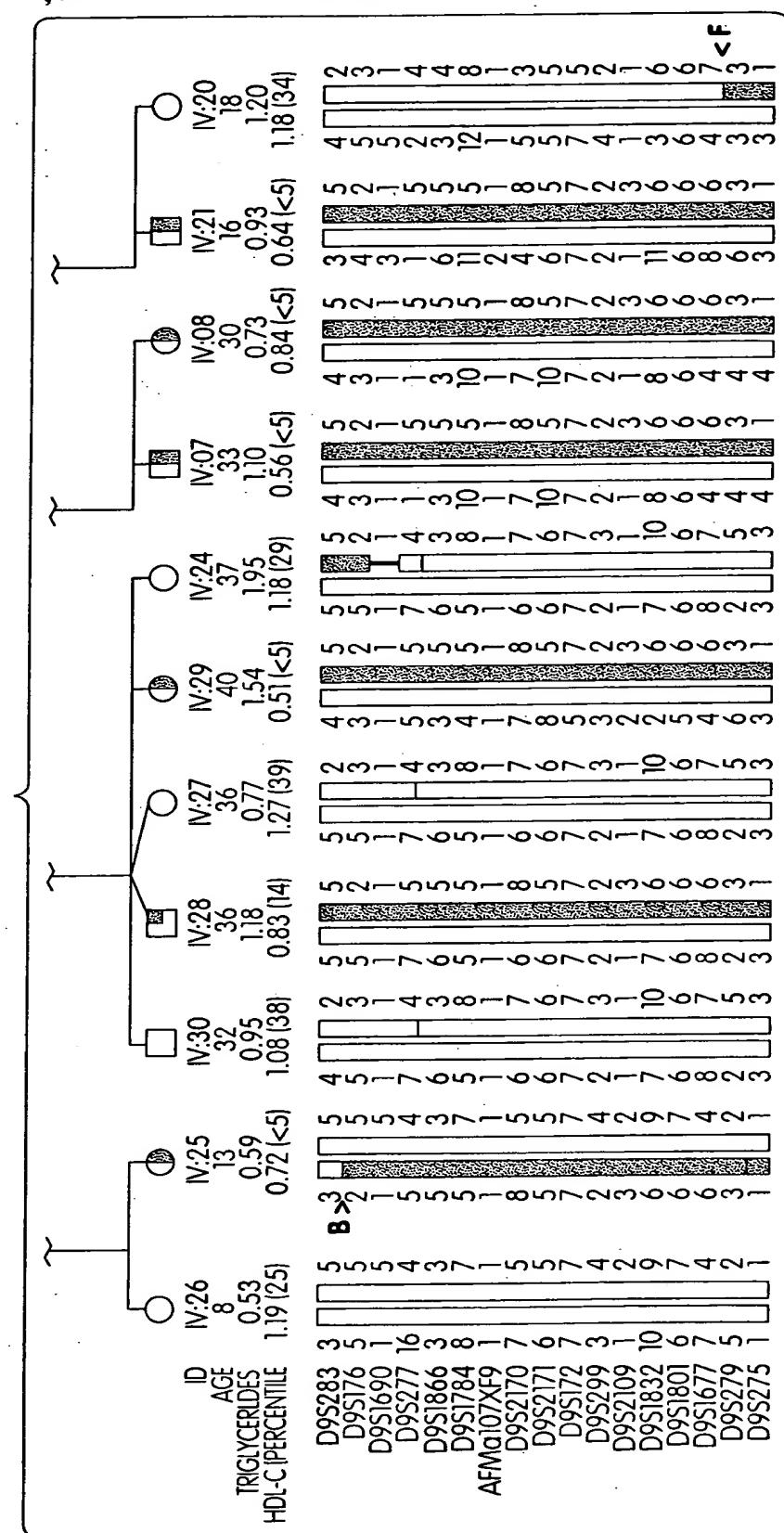


Figure 2B – (2)



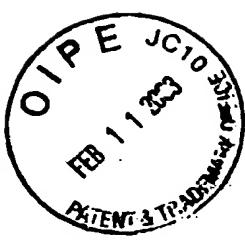
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**Figure 10A**



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			1.4
			1.6
			1.6
			1.4
			1.4
			3
			1.5
			1.5
			>0.9
			0.944 (\\)
			>0.9
			1.062 (/6.5)
			>1.0
			1.475
			1.475
			1.5
			0.522
			0.5
			1.228
			1.2
			>1.898 (2)
			2
			0.112
			0.1
			1.545
			1.5
			1.087
			1.1
			0.265
			0.3
			>0.622 (0.9)
			0.9
			0.909
			0.9
			2.355
			2.4
			0.372
			0.4
			>1.059 (1.3)
			1.3
			0.483
			0.5
			0.659
			0.7
			0.941
			>1.075
			167
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			96
			95
exon	26	114	GTTTGTGCGAGATGGGGAAAG
exon	27	149	CACCAAGAACAGGAGCATGG
exon	28	125	TCTGACTCTGATGGGAATTGC
exon	29	99	GCCGTGTCACAGAGAAATTGCTT
exon	30	190	TTACCGGAATGTATCCTGGCTC
exon	31	95	AGTCAGGTTCCGGTCAACAC
exon	32	33	CCGGTCCTTATATCCCTCAGGTG
exon	33	106	CCTTGTAACACACTCCGACTGA
exon	34	75	TGTTGTCACAGGTTGCCAGA
exon	35	170	TGAGGTTTATGGGGATGTT
exon	36	178	ATGGTTTTCCTTGGCTGTC
exon	37	116	ATCTGCCTTTCCTTGTCTGA
exon	38	145	AGGGAGGTGCAACAGTGGATA
exon	39	124	TCACTCCOATATTTCAGAACCTGA
exon	40	130	TGTTTATTGAGATGGCTGAA
exon	41	121	CGTTAGAGACTGAATCTTGTCTG
exon	42	63	AGTCCTGCCTTCCACAGTGT
exon	43	107	GGTAGTTAACGTGTAGGGCA
exon	44	142	CAGGAACATTAGGGCAGATTG
exon	45	135	CATGTATCTGTAGGACAGATGA
exon	46	104	CTGTTCAAAAGATGGCTCTGC
exon	47	93	CCTAGGAACCTGGAAATGCTG
exon	48	244	GGGTCCCAGGGTTCACTGTAT
exon	49	295	CTTGACCTTAATTCACATCTGG

Figure 10B



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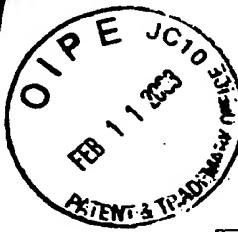
ERRORS IN PUBLIC SEQUENCE (differences between samples and Genbank entry AJ012376.1):			
Exon/Intron	Nucleotides	Amino Acid Change	Sequence difference/context
2	T150C A152G	no change	Public sequence: TGTCAAGCTGGTTACTCGGAAGTCG Correct sequence: TGTCAAGCTGGCTGCTGGAAGTGG
7	C839T	no change	Public sequence: AGGAGCTGGCCGAAGGCCACAA Correct sequence: AGGAGCTGGCTGAAGGCCACAA
33	C4738T	T1495I	Public sequence: AATGATGCCACAAACAATG Correct sequence: AATGATGCCATCAAACAATG
35	C5017T	P1588L	Public sequence: GAGGTGGCTCCGATGACCACA Correct sequence: GAGGTGGCTCTGATGACCACA
43	G5995A	R1914K	Public sequence: TTCCTTAACAGAAATTAGTATC Correct sequence: TTCCTTAACAAAAATTAGTATC
48	C6577T	P2108L	Public sequence: CGAAAGTTCCAAAAGAGAAA Correct sequence: CGAAAGTTCTAAAAGAGAAA
49	G6899A	not applicable	Public sequence: AGTAAAAGGGACTAGACTTT Correct sequence: AGTAAAAGGGAAACTAGACTTT
Mutations:			
13	A1864G	Q597R	More common: GCCTACTTGGAGGATGTCGTC Less common: GCCTACTTGGGGATGTCGTC
14	delta C/T 2151-3	delta I093	More common: CCTCATTCCTCTCTCTTGAGCG Less common: CCTCATTCCT/CCTGTGAGCG
15	G2385A	V771W	More common: GCAGGACTACGTGGCTTCAC Less common: GCAGGACTACATGGCTTCAC
18	C2799T	R909STOP	More common: AAAAGCTTACCGAGATGGAT Less common: AAAAGCTTACTGAGATGGCAT
18	C2860T	I929T	More common: GGCCAGATAACCTCTTCCTG Less common: GGCCAGATACTCTCTTCCTG
22	T3346C	M1091T	More common: ACACACACATGGATGAAGCG Less common: ACACACACGGATGAAGCG

Figure 11A



Intron 24	[+1] G to C splice donor site length	Altered transcript	More common: Less common:	CCTGGAAAGTAAGTAACT CCTGGAAAGTAAGTAACT	194 195
30	T4503C	C1477R	More common: Less common:	GCTGCCCTGTTGCCCCCAGG GCTGCCCTGTTGCCCCCAGG	196 197
35	GG 4958-57 to C	Frame shift at aa 1628	More common: Less common:	TAGCCATTATCGMAATTACTCT TAGCCATTATCGMAATTACTCT	198 199
41	delta AAGATG 5752-7	delta(E.D.)1893-1894	More common: Less common:	GATGAAGATGAGATGAGGGGG GATGAAGATG/TGAGGCCCCAA	200 201
48	C6504T	R2144Stop	More common: Less common:	AATAGTGTACGAAATAGCCGG AATAGTGTACGAAATAGCCGG	202 203
Promoter Variants:					
Location	Position Relative to Xenon cDNA	Position Relative to SEQ ID NO: 14 Containing Exon 1		SEQ ID NO:	
1	G57C	8216	More common: Less common:	ACACCCCTGGGGGGGGGGGGGG ACACCCCTGGGGGGGGGGGGGG	204 205
5	(-)4 ins. G	8158	More common: Less common:	GACCAAGCCACGGGCTCCCTG GACCAAGCCACGGGCTCCCTG	206 207
5	A (-)380 G	7780	More common: Less common:	CATTTCCTTAAACAGACGT CATTTCCTTAAACAGACGT	208 209
5	A (-)479 C	7681	More common: Less common:	GAATAATTAGTATGTAAGGAAG GAATAATTAGTATGTAAGGAAG	210 211
5	A (-)738 G	7422	More common: Less common:	CCTTCGCCTGCCAGGTTCAGGGATT CCTTCGCCTGCCGGTTTCAGGGATT	212 213
5	A (-)1045 G	7115	More common: Less common:	TATGTGCTGACCATGGGAGCTTGT TATGTGCTGACCGTGGGAGCTTGT	214 215
5	A (-)1113 G	7047	More common: Less common:	GTGACACCCAACGGGAGTAGGG GTGACACCCGAGGGAGTAGGG	216 217
5	(-)1181 ins. CCCT	6979	More common: Less common:	AGTATCCCT/TGTTACCGAGAA AGTATCCCTCCCTGGTCACGAGAA	218 219

Figure 11B



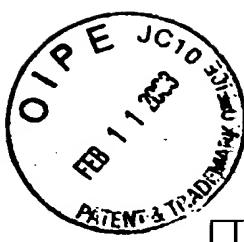
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Polymerisms:	Nucleotides	Amino Acid Change	Sequence difference/context	SEQ ID NO:
5	G548A	no change	More common: CTGGTTCTGTATCACAAACC Less common: CTGGTTCTTATCACAAACC	220 221
6	G730A	R219K	More common: GGCCTAACAGGGAGAAACTG Less common: GCCTAACAAAGGAAACTG	222 223
Intron 7	G(+)2383 T	Not applicable	Allele 1: TTAAAGGGGGTATTAGGA Allele 2: TTAAAGGGGTATTAGGA	224 225
Intron 7	G(+)3035 T	Not applicable	Allele 1: GAAGAATTGTTTGTATTGATT Allele 2: GAAGAATTTTTTTGTATTGATT	226 227
8	C101T	no change	More common: GCCGCCATCCGAGGAGGG Less common: GCCGCCATCTGAGGAGGG	228 229
8	G102A	no change	More common: ACGGAGGGGGCTGAGATCA Less common: ACGGAGGGGGACTGAGATCA	230 231
Intron 9	(-)42 ins. G	Not applicable	More common: ACGACCAAACGCTTGT Less common: ACGACCAAACGCTTGT	232 233
Intron 13	T(+24 A	Not applicable	More common: AAGCCACTTTTAACCACT Less common: AAGCCACTGTTAACCACT	234 235
15	A2394C	T774P	More common: CGTGCGCTTCACCTGAGAT Less common: CGTGCGCTTCACCTGAGAT	236 237
15	G2402C	K776N	More common: TCACACGAGTCCTCGCTG Less common: TCACACGAGTCCTCGCTG	238 239
Intron 14	C(+16 T	Not applicable	Allele 1: GGAGCCCTAACCCGTTTCCC Allele 2: GGAGCCCTAACCTGGCTTCCC	240 241
17	A2723G	I883W	Allele 1: AGAGAGATAATCAGAACT Allele 2: AGAGAGATAATCAGAACT	242 243
Intron 17	C(+)2000 G	Not applicable	Allele 1: GGCGAGTCGCTGCTGCTGCTTA Allele 2: GGCGAGTCGCTGCTGCTGCTTA	244 245

Figure 11C



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21	T3233G	no change	More common: Less common:	GATCTAAGCTTCATTCCTGG GATCTAAGCTTCATTCCTGG	246 247
Intron 21	G(+)-118 T	Not applicable	Allele 1: Allele 2:	CCTCTCTCTTACCAAGAA CCTCTCTCTTACCAAGAA	248 249
Intron 21	A(+)-1563 G	Not applicable	Allele 1: Allele 2:	CATTCTAGGGATCATAGCCAT CATTCTAGGGATCATAGCCAT	250 251
Intron 24	G(+)-321 T	Not applicable	Allele 1: Allele 2:	AAGTACACTGGAGAACAGGG AAGTACAGTGAGGAACAGGG	252 253
Intron 29	A(-)-624 G	Not applicable	Allele 1: Allele 2:	AATTCCCTAAATAGAAATGCA ATTCCCTAAATAGAAATGCA	254 255
Intron 31	T(+)-30 C	Not applicable	More common: Less common:	GGCCCCCTGCCCTTATTATTACT GGCCCCCTGCCGTATTATTACT	256 257
Intron 33	A(+)-732 G	Not applicable	Allele 1: Allele 2:	TAAGAGAATTACTTGAACCCGG TGAGAGAATTACTTGAACCCGG	258 259
Intron 33	C(+)-898 T	Not applicable	Allele 1: Allele 2:	TTTGGCTGAAACAAATCACTGCA TTTGGCTGAAATATCACTGCA	260 261
Intron 34	C(+)-234 T	Not applicable	Allele 1: Allele 2:	AACCTCACTGCTCCCTCATCTG AACCTCACTTCCCTCATCTG	262 263
34	G4834A	R158TK	More common: Less common:	CTGGACACCGAAATAATGTC CTGGACACCAAATAATGTC	264 265
37	C 5266G	S1731C	More common: Less common:	TCCTATGATGCTCCACCAAT TCCTATGATGCTCCACCAAT	266 267
Intron 43	T(+)-118 C	Not applicable	More common: Less common:	AAGAAGTGGCTTGATTTGC AAGAAGTGGCTTGATTTGC	268 269
Intron 43	C(+)-1665 G	Not applicable	Allele 1: Allele 2:	AACTGATTTGATGGATAGCTG AACTGATTTGATGGATAGCTG	270 271
48	C6521T	no change	More common: Less common:	CAGGGTCCAACCCGACCTGA CAGGGTCCAATCCGGACCTGA	272 273
Intron 10	(+)-14 118. T	Not applicable	More common: Less common:	GGGTCAGGATGGGACAG GGGTCAGGATGGGACAG	284 285
Exon 16	G2547A	V8251	More common: Less common:	CCACTTGGCTCATG CCACCTGATTCATG	286 287
Polymorphism in an ABC1 BAC contig: This polymorphism is within approximately 200kb of the ABC1 gene					
SEQ ID NO: 274 275					
A or G					
Allele 1: Allele 2:					
TTCGGAGGCTAACCCAGGAGA TTCGGAGGCTAACCCAGGAGA					

Figure 11D



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### Genomic contig containing ABC1 exon 1:

Underline = putitive promotor element

## **Figure 12A-(1)**



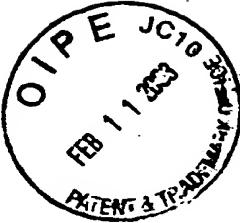
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## **Figure 12A-(2)**



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## **Figure 12A-(3)**



SEQ ID NO: 15

Genomic contig containing ABC1 exon 2:

ctttttttttttttttttttttttttttgaggtaagtctcactctgttgcggcaggctggagtgcaatggagcgatc  
ttggctcaccccaacctctgttcctgggttcaaacagttctcgcctcgcctcccaggtagctggattacaggctc  
ccgcccaccatgcccagctatTTTGTatTTTCTAGTAGAGATGGGTTACCCCTTGACCAGGCTGGTCTGAACTC  
ctgacctcatgtcaacccacccatgcctccaaagtgtctggattacaggtagccaccacgccccgcctcataagt  
atTTCTAAATTATTTACAGTCATGCCATTAAAAGGAAAGTTGTATTCTGTCTTGTAAATTATAAGTATT  
attcagctacaagcttggatggcatataattttgtattctgttttacttaatattacatggctaattgattctgt  
gtttcataaacattattctgtatgtatggcatatatgtttagtacatgtaccataattgaatcattccctattgcta  
tgcaattaagtgttccaatattttcaattataatgttcaatgaatgaataactttatgcataatgttttat  
cttaagttcagttccatggatgaattccaggaaatgtatggcaaatgggataaacatgactcttgaataatgtt  
gttaacattgtttccaaaggctcaactgtattatattccgtttcattatTTTAACCAGCTTACTTACCTCACC  
aaacatTTTAAAGCATTATCATGTGGTAGGTTAGAAGAAGAAAGTGTACCTAAGGGAGAAGCTTATATAAAG  
gttccctgtgtaccaagtgtatacagacacaaagtacctggggaaattgagatgaggagtcctggctcagctggga  
aaaaagttcatTTTCAAGAGTCATGGTTGTTGGCAGAAAGAAAATTGCTTCCCACCCCCACCCCCAC  
tttatttaggtataattgacaataaaattgtatatttttaagatatgcataatgtatatatgtatatctcaacttaa  
aaaataagctacagaataaaagggtttctttagatTTTAAAGAAAAGGCTGAATGTCACTCCAAAGCTTGGAAATT  
gagttgtgtcctttggattatTTTACAGAAATTAGCAAGACCAGCCCCATTTGGTCTTGTAGTACTCCACTGTC  
agcatgtttccatggatccatTTGCCTTATTTCATTCTGTGCGTCTATGCAAACATTCTTGATA  
gtttatgttaacagtgtttttgttccatggatTTTACAGAAATTATACATGCTTGTGAAATTAGAAAAGACAGGAA  
agtattaaaacatcmcytt  
ggagtgcagtggcgtatctcagtcacagcaaccccgctccaggTTAAGTGTATTCTCTGCCTCAGCCTCCAAAG  
tagctggagtacaggcatgcaccaccacgccccgtaattttgtatttttagtagagatgggTTTACCATGTTGGCC  
aggctgtctcaaactcctgacactcaggtatccgcctgcctggcctcgaaaggTCTGGATTATAGCAGGAGGCC  
tgcgccaggcacacacgttttatcatcctagtacatccactgtcattatTTGCTGTATTCTCTGCCAGTC  
actctgatcatgcagtggcgtatgcagtgtatcggctactgcacacccatggcTTCTGGTTGAGTGTATTCTCC  
tgccttagctcctgggtcaagtgtattctgcctggcctccaaagttagctggattacaggcataacccccatgc  
ccatctaattttgtatttttagacacacgcttcaactaaattttgtatttttagtagagatgggTTTACCATG  
ttggccaggctggctccaactcctgacgtgtatccgcctgcctggcctcacaaggTCTGGATTACAGGCATGAGCCA  
ctgcatccatgcccaaaagatTTTAAAGAGTTAATGTTAGAACCATAAAGGTCTTGGAAATAAAAACAGTT  
ttttaaaatatacagaataaaacaacaataaaaataaaaacacccaaaacaatctgaagcacgacacccatg  
cagaaaggTTCAATTATGATCTATTCAAGTGGAAATATCAAGTAGACACATTACAGGACATTTAAGATTATTTA  
tgtcatggaaatgtctccaggatgtttaatgaaaaacagaatacaaaaggatataatgtctgcataatctcaata  
ttgttagaaaaatattattatgtatgcataaaaaagacaaaaggatTTAAGAGATCATTGTACTTCAGTTA  
ctaggatgtctggaggtaggatTTAGGTGTTATATTACCTTTAAACTTTCTGTATTTTTATTTC  
atTTTCCATAAAAATATAAGGACTGAAGATCAAGAAAAATTCTGCTTGGCTCAGTCAGTCAGTCACGCCCTGTAATC  
ccagcagTTGGAGCCCTAGGGAGAGGATCACTGAACCCAAAGAGTTGACGTTCCAGTGAGCTATGATCTCCGGATC  
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aggcagtgttaacttagtgcataacactactggctcaattatattgtgttagtattccatctgtccgtctgtaat  
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gaagttcaatgtatTTTAAACTCATCGGAGAAGATGATGACCGAGACCTGGACAGATGGGAAGGACTTGCACTCTC  
tttacagtctgatgcacacaggtaatggaaactatgtgtgaattttcattgtctttgagagcccttctctgccc  
cataggagcagcttggatgtcaatttagaggagcaagggttggatTTAGCACAGCAGGGTGGCCTGGTCTCT  
ctcaacatagtcaccacatacctggcactatgtaaggctggaaatgcagacagatgggtgcctgcttcaagtgctca  
atgtgctgaggaagccagcaacagaaacagatgattcaggagctccaggaaaatgtctacaggaggatgtgcctgggtt

Figure 12B - (1)



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actggagtagcacaggaggaggcttctagctcaggctgagattttagtaaaggaaattatgccacgatgaatcctgaag  
aatgaatagaagtgaaccagataaaggcacatggactccaaacagttctgttaaagcttagagagtggtggagagactggagaagttgattaat  
gttatgttaaaagggtggactccaaacagttctgtttaaagcttagagagtggtggagagactggagaagttgattaat  
tagtaaatgaagtgtctgtggattccagatcccagtggatccatatttttaaatttacagtgttct  
atcttattccactcagTGTCAGCTGCTGGAAAGTGGCCTGGCCTATTTATTCCTGATCCTGATCTGTTCG  
GCTGAGCTACCCACCCCTATGAACAACATGAATgtaaactgtggatgtgcctgagactcaccaatggcaggaaaat  
ccaggcaattaacgtggctaaattggactttccaaagatgctgtttggaaacatcacatgcttggatcagaa  
aacctaggcttctaatttgtataaggcatgaactcaggagactgtttcagtcctagtgaatggtgataattgttaatt  
ataacagttagacaacatctctttacacatttaatcatgaaaatagaataacctactgataatttagaaagtggtg  
attaaaagcacatttaagataatgccttaacacctagtctttccatatgcatgtcttaatcacacattgcaaatca  
tggAACACAGAAATT

**Figure 12B - (2)**



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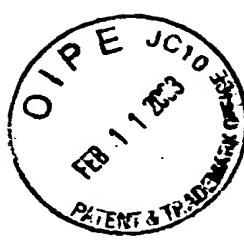
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SEQ ID NO 16

### Genomic contig containing ABC1 exon 3:

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caacatttacgttagctggaatgttagctggacttcagttactgccttagtgatccccatccactaagcagctca  
gtccatacccctacgagaccacacaagcttatgagatactgttcttcaggaaagcagtgccggccaccccttaat  
tgtgttcttggcctggccatcttctacaatatatacgaaatcgatcttgcctgatccatgcacatcac  
acatgtcatattaaac  
tgatttcataaaaaaaagaaaaagagcggccaggcacagtgccggatctgatccatggatcttgcctgatcc  
aaaccagcctggccaacacgggtggaaacctcgctctactaaaaataaaaattagccaggcgtggcgcacac  
aatcccagctactggggaggctgaggcaggagaattgctcaacctgcgaggctgagttcagtgagccgagattgc  
cattgactccagcctggcaacagactgagactctgtctaaaaaaaaaaaaaaaagcataaactgaaat  
tatgcaatttatgcctgtgagataattctgtttcttttggaaacccaaagagatttttgattgatgagcaa  
acattttagatttatatacgattatgccaagcaccactgaagtataagttcaagggcaaactcagtttcatcta  
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**Figure 12C - (1)**



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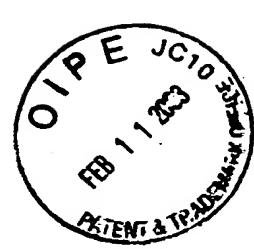
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## Figure 12C - (2)



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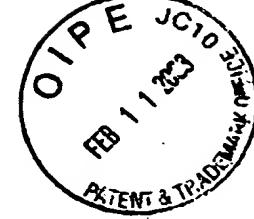
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SEQ ID NO 17

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Figure 12D



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SEQ ID NO 18

### Genomic contig containing ABC1 exon 5:

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## **Figure 12E**



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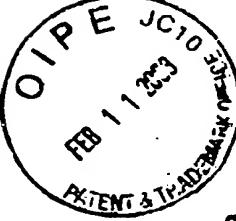
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**SEQ ID NO 19**

### **Genomic contig containing ABC1 exon 6:**

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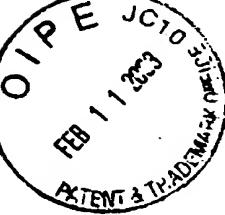
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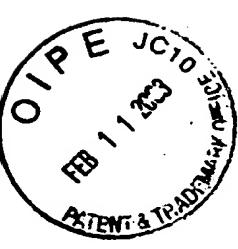
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### Genomic contig containing ABC1 exon 8:

## **Figure 12G - (1)**



## **Figure 12G - (2)**



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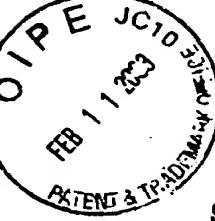
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Figure 12G - (3)



SEQ ID NO 21

## Genomic contig containing ABC1 exon 9 through 22

**Figure 12H - (1)**

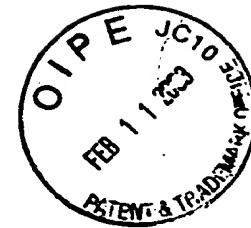


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## **Figure 12H - (2)**



## **Figure 12H - (3)**



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**Figure 12H - (4)**

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Figure 12H - (5)



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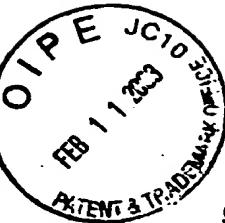
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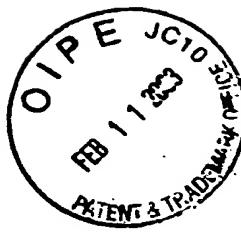
**Figure 12H - (6)**



SEO ID NO: 22

Genomic construct containing ABC1 exon 23 to 28

**Figure 12 I - (1)**



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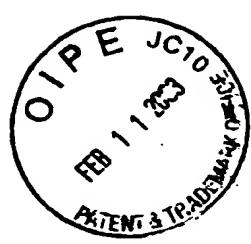
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Figure 12 I - (2)



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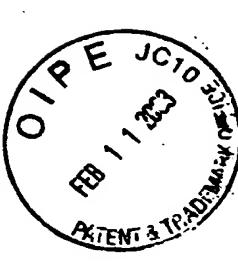
61/76

SEQ ID NO: 23

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**Figure 12J**



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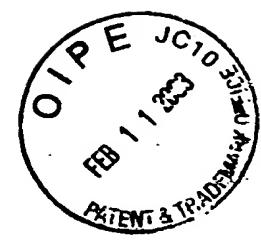
FEB 1  
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62/76

SEQ ID NO: 24

Genomic contig containing ABC1 exon 30 and 31:

## **Figure 12K**



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TECH CENTER 1600/2900

63/76

SEQ ID NO: 25

Genomic contig containing ABC1 exon 32:

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## Figure 12L



64.76

SEQ ID NO: 26

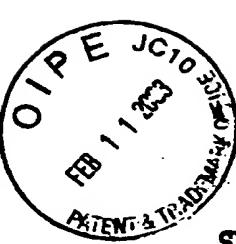
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## **Figure 12M – (2)**



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SEQ ID NO: 27

Genomic contig containing ABC1 exon 37 to 41:

## **Figure 12N – (1)**



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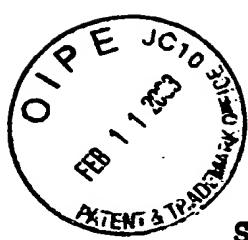
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ttgtcctgaaaaatagttgaaaggttcattttcttgcattttccccaagACCTGTAAATGCAAAGCTATCTCCTCTG  
AATGATGAAGATGAAGATGTGAGCCGGAAAGACAGAGAATTCTTGATGGTAGGCCAGAATGACATCTAGAAATCAA  
GGAGTTGACGAAGgtgagagagatcacaggttacaatagctcatcttcagtttttcagtttatgtgctgtcaacccagca  
gtttgctgacttgctaataaaaggcatgtgtccaaaatgtacatctataccagggtctgtcaattttatttaaa  
aacaccatggagacttcttaagaattttacttgagaattttgtatgtatgtatctgtcaaactgagtagagagataatgg  
tatatgcttacatttatgtgttagttataaaacatactaataattgtatctgtcaaactgagtagagagataatgg  
gatt

## Figure 12N – (2)



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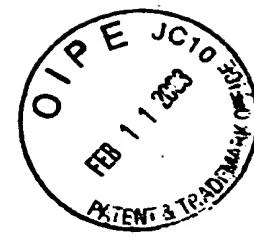
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SEQ ID NO: 28 ~~TECH~~  
Genomic contig containing ABC1 exon 42 to 45:

## **Figure 12O – (1)**



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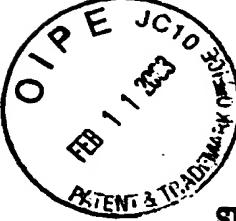
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gattgtctaaccagagtatctcacctgctaaaatctaagttagtttcttccttgagTATCTTATCAAACATCCA  
TGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTGATGCCATCACAGAGCTGTTGACTGGGAGAGAACACGTGGAGT  
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gtgatttgcattttctgttagataagacattgttgcattttgcattccctgaaaatgaagagtgtggacacagct  
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## Figure 12O – (2)

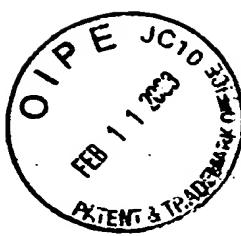


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SEQ ID NO.: 29

## Genomic contig containing ABC1 exon 46 to 49

## **Figure 12P – (1)**



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## **Figure 12P – (2)**

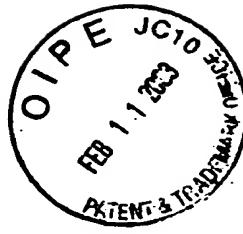


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No.	Name	Location in SEQ ID No. 14	Sequence	Strand Length	
1	PPRE	58-69	ACGTTAAAGTCA	12	Complement
2	PPRE	1997-2009	AGAGTAGAGGGCA	13	Lead
3	PPRE	2150-2161	ATGTCAGGTCA	12	Lead
4	PPRE	2156-2169	AGTTCAAAAGGCCA	14	Lead
5	PPRE	4126-4139	AGGCAGGAAGGGCC	14	Complement
6	PPRE	5075-5087	AGGGCAGAACTGA	13	Lead
7	PPRE	6604-6615	ATGCCAAAGGTCA	12	Complement
8	PPRE	6731-6743	GGGGCGAGGTA	13	Complement
9	PPRE	7220-7233	AGGTAAATGAGGACA	14	Complement
10	PPRE	7554-7568	GGATCACGAGGTCA	15	Complement
1	SRE	159-166	CAGCCCCAT	8	Lead
2	SRE	1133-1140	CAGCTCAC	8	Complement
3	SRE	1145-1152	CACACCAC	8	Lead
4	SRE	1809-1816	CAGCCCTC	8	Complement
5	SRE	1894-1901	CAGCCCCAT	8	Lead
6	SRE	2563-2570	CAACCCAC	8	Lead
7	SRE	3303-3310	CAGCTCAC	8	Lead
8	SRE	3470-3477	CGGCCAC	8	Complement
9	SRE	4784-4791	CTCCGCAC	8	Complement
10	SRE	4802-4809	CTGCCCTAC	8	Complement
11	SRE	4970-4977	CACCTCAC	8	Complement
12	SRE	6487-6494	CAAGCTTAC	8	Complement
13	SRE	6565-6572	CACCCAAC	8	Complement
14	SRE	6727-6734	CACCCCTCA	8	Lead
15	SRE	7041-7048	CAACCCAC	8	Lead
16	SRE	8059-8066	CGGCCCTC	8	Complement
1	ROR (retinoic acid receptor related)	166-172	AGGGTCA	7	Complement
2	ROR (retinoic acid receptor related)	166-173	AAGGGTCA	8	Complement
3	ROR (retinoic acid receptor related)	263-370	ATGGGTCA	8	Lead
4	ROR (retinoic acid receptor related)	264-370	TGGGGTCA	8	Lead
5	ROR (retinoic acid receptor related)	2218-2225	TAGGGTCA	8	Lead
6	ROR (retinoic acid receptor related)	22219-2225	AGGGTCA	7	Lead
7	ROR (retinoic acid receptor related)	3643-3649	TGGGTCA	7	Lead
8	ROR (retinoic acid receptor related)	6604-6610	AAGGTCA	7	Complement
1	SREBP-1 or "E box"	473-479	ACACCTG	7	Complement
2	SREBP-1 or "E box"	536-541	ACACATG	7	Lead
3	SREBP-1 or "E box"	537-543	TCATG TG	7	Complement
4	SREBP-1 or "E box"	6555-6611	TCATG TG	7	Complement
5	SREBP-1 or "E box"	925-931	ACACTG	7	Lead
6	SREBP-1 or "E box"	967-973	TCAC T G	7	Complement
7	SREBP-1 or "E box"	968-974	TCAA GTG	7	Complement
8	SREBP-1 or "E box"	1053-1069	ACAGGTG	7	Complement
9	SREBP-1 or "E box"	1104-1110	TCAC T G	7	Complement
10	SREBP-1 or "E box"	1105-1111	TCAAGTG	7	Complement
11	SREBP-1 or "E box"	1561-1567	TCAC T G	7	Lead

Figure 16A



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TCAAAATG	1670-1676
ACACTTG	1748-1754
ACAAGTGC	1749-1755
TCATGTC	1858-1859
ACAAATG	1899-1905
ACACGTG	2393-2399
ACACCTG	2199-27005
TCACATG	2697-27083
ACAACTG	2740-2746
ACACATG	2969-5975
TCACCTG	2979-2985
ACACATG	2981-2987
ACATGGT	2980-2986
ACACATG	2982-2988
TCACCTG	3461-3467
ACACATG	3462-3468
TCACCTG	3547-3553
ACACATG	3752-3758
TCACCTG	4226-4232
ACACGTG	4582-4588
TCAGTTG	4588-4594
TCAGCTG	4861-4867
ACAAATG	4951-4957
TCACATG	5096-5102
ACACATG	5913-5919
ACACATG	6245-6251
TCACCTG	6288-6294
ACACATG	6623-6629
TCACCTG	6837-6843
ACACATG	7032-7038
TCACCTG	7069-7075
ACACATG	7101-7107
TCACCTG	7138-7144
ACACATG	7139-7145
TCACCTG	7240-7246
ACACATG	7467-7473
TCACCTG	7640-7646
ACACATG	7641-7647
TCACCTG	7653-7659
ACAAATG	7738-7744
TCACCTG	7889-7896
TCACCTG	7805-7807
TCACCTG	8052-8058

**Figure 16B**